

## SEQUENCE LISTING

<110> John A. Chiorini  
Michael Schmidt  
Ioannis Bossis  
Di Giovanni Pasquale

<120> Bovine Adeno-Associated Viral (BAAV)  
Vector and Uses Thereof

<130> 14014.0417U2

<150> PCT/US04/40825

<151> 2004-12-06

<150> 60/526,786

<151> 2003-12-04

<160> 23

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 4694

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic  
construct

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<211> 1833

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic construct

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cgcgtgttcc	tgtacgagtg	gaacaaattt	tccaagcagg	agagcaaatt	ctttgtgcag	240
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<210> 3

<211> 610

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic construct

<400> 3

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Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Asn	Phe	Val	Asp	Trp	Val	Thr	Gly
			20					25					30		
Gln	Ile	Trp	Glu	Leu	Pro	Pro	Glu	Ser	Asp	Leu	Asn	Leu	Thr	Leu	Ile
			35					40					45		
Glu	Gln	Pro	Gln	Leu	Thr	Val	Ala	Asp	Arg	Ile	Arg	Arg	Val	Phe	Leu
			50					55					60		
Tyr	Glu	Trp	Asn	Lys	Phe	Ser	Lys	Gln	Glu	Ser	Lys	Phe	Phe	Val	Gln
					70					75					80
Phe	Glu	Lys	Gly	Ser	Glu	Tyr	Phe	His	Leu	His	Thr	Leu	Val	Glu	Thr
					85					90					95
Ser	Gly	Ile	Ser	Ser	Met	Val	Leu	Gly	Arg	Tyr	Val	Ser	Gln	Ile	Arg
					100					105				110	
Ala	Gln	Leu	Val	Lys	Val	Val	Phe	Gln	Asn	Ile	Glu	Pro	Arg	Ile	Asn
					115					120				125	

Asp	Trp	Val	Ala	Ile	Thr	Lys	Val	Lys	Lys	Gly	Gly	Ala	Asn	Lys	Val	130	135	140
Val	Asp	Ser	Gly	Tyr	Ile	Pro	Ala	Tyr	Leu	Leu	Pro	Lys	Val	Gln	Pro	145	150	155
Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Leu	Glu	Glu	Tyr	Lys	Leu	Ala	Ala	165	170	175
Leu	Asn	Leu	Glu	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	Phe	Gln	Leu	Glu	180	185	190
Ser	Ser	Gln	Arg	Ser	Gln	Glu	Ala	Ser	Ser	Gln	Arg	Asp	Val	Ser	Ala	195	200	205
Asp	Pro	Val	Ile	Lys	Ser	Lys	Thr	Ser	Gln	Lys	Tyr	Met	Ala	Leu	Val	210	215	220
Ser	Trp	Leu	Val	Glu	His	Gly	Ile	Thr	Ser	Glu	Lys	Gln	Trp	Ile	Gln	225	230	235
Glu	Asn	Gln	Glu	Ser	Tyr	Leu	Ser	Phe	Asn	Ser	Thr	Gly	Asn	Ser	Arg	245	250	255
Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Ser	Lys	Ile	Met	Ser	Leu	260	265	270
Thr	Lys	Ser	Ala	Ser	Asp	Tyr	Leu	Val	Gly	Gln	Thr	Val	Pro	Glu	Asp	275	280	285
Ile	Ser	Glu	Asn	Arg	Ile	Trp	Gln	Ile	Phe	Asp	Leu	Asn	Gly	Tyr	Asp	290	295	300
Pro	Ala	Tyr	Ala	Gly	Ser	Val	Leu	Tyr	Gly	Trp	Cys	Thr	Arg	Ala	Phe	305	310	315
Gly	Lys	Arg	Asn	Thr	Val	Trp	Leu	Tyr	Gly	Pro	Ala	Thr	Thr	Gly	Lys	325	330	335
Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ser	His	Thr	Val	Pro	Phe	Tyr	Gly	Cys	340	345	350
Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	Cys	Val	Glu	Lys	355	360	365
Met	Leu	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ser	Lys	Val	Val	Glu	370	375	380
Pro	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Arg	Val	Arg	Val	Asp	Gln	Lys	385	390	395
Cys	Lys	Ser	Ser	Val	Gln	Val	Asp	Ser	Thr	Pro	Val	Ile	Ile	Thr	Ser	405	410	415
Asn	Thr	Asn	Met	Cys	Val	Val	Val	Asp	Gly	Asn	Ser	Thr	Thr	Phe	Glu	420	425	430
His	Gln	Gln	Pro	Leu	Glu	Asp	Arg	Met	Phe	Arg	Phe	Glu	Leu	Met	Arg	435	440	445
Arg	Leu	Pro	Pro	Asp	Phe	Gly	Lys	Ile	Thr	Lys	Gln	Glu	Val	Lys	Asp	450	455	460
Phe	Phe	Ala	Trp	Ala	Lys	Val	Asn	Gln	Val	Pro	Val	Thr	His	Glu	Phe	465	470	475
Met	Val	Pro	Lys	Lys	Val	Ala	Gly	Thr	Glu	Arg	Ala	Glu	Thr	Ser	Arg	485	490	495
Lys	Arg	Pro	Leu	Asp	Asp	Val	Thr	Asn	Thr	Asn	Tyr	Lys	Ser	Pro	Glu	500	505	510
Lys	Arg	Ala	Arg	Leu	Ser	Val	Val	Pro	Glu	Thr	Pro	Arg	Ser	Ser	Asp	515	520	525
Val	Pro	Val	Glu	Pro	Ala	Pro	Leu	Arg	Pro	Leu	Asn	Trp	Ser	Ser	Arg	530	535	540
Tyr	Glu	Cys	Arg	Cys	Asp	Tyr	His	Ala	Lys	Phe	Asp	Ser	Val	Thr	Gly	545	550	555
Glu	Cys	Asp	Glu	Cys	Glu	Tyr	Leu	Asn	Arg	Gly	Lys	Asn	Gly	Cys	Ile	565	570	575
Phe	His	Asn	Ala	Thr	His	Cys	Gln	Ile	Cys	His	Ala	Val	Pro	Pro	Trp	580	585	590
Glu	Lys	Glu	Asn	Val	Ser	Asp	Phe	Asn	Asp	Phe	Asp	Asp	Cys	Asn	Lys	595	600	605

Glu Gln  
610

<210> 4  
<211> 1173  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note=synthetic  
construct

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atgttcagat ttgaactcat gcggcggtc ccgccagatt ttggcaagat taccaagcag 720  
gaagtcaaa acttttttgc ttgggcaaag gtcaaccagg tgccggtgac tcacgagttt 780  
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<210> 5  
<211> 390  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note=synthetic  
construct

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Gly Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys  
35 40 45  
Ile Met Ser Leu Thr Lys Ser Ala Ser Asp Tyr Leu Val Gly Gln Thr  
50 55 60  
Val Pro Glu Asp Ile Ser Glu Asn Arg Ile Trp Gln Ile Phe Asp Leu  
65 70 75 80  
Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Val Leu Tyr Gly Trp Cys  
85 90 95  
Thr Arg Ala Phe Gly Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala  
100 105 110  
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ser His Thr Val Pro  
115 120 125

Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
130						135					140				
Cys	Val	Glu	Lys	Met	Leu	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ser
145					150					155					160
Lys	Val	Val	Glu	Pro	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Arg	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Val	Gln	Val	Asp	Ser	Thr	Pro	Val
			180					185					190		
Ile	Ile	Thr	Ser	Asn	Thr	Asn	Met	Cys	Val	Val	Val	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Glu	Asp	Arg	Met	Phe	Arg	Phe
		210				215					220				
Glu	Leu	Met	Arg	Arg	Leu	Pro	Pro	Asp	Phe	Gly	Lys	Ile	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Ala	Trp	Ala	Lys	Val	Asn	Gln	Val	Pro	Val
				245					250					255	
Thr	His	Glu	Phe	Met	Val	Pro	Lys	Lys	Val	Ala	Gly	Thr	Glu	Arg	Ala
			260					265					270		
Glu	Thr	Ser	Arg	Lys	Arg	Pro	Leu	Asp	Asp	Val	Thr	Asn	Thr	Asn	Tyr
		275					280					285			
Lys	Ser	Pro	Glu	Lys	Arg	Ala	Arg	Leu	Ser	Val	Val	Pro	Glu	Thr	Pro
		290				295					300				
Arg	Ser	Ser	Asp	Val	Pro	Val	Glu	Pro	Ala	Pro	Leu	Arg	Pro	Leu	Asn
305					310					315					320
Trp	Ser	Ser	Arg	Tyr	Glu	Cys	Arg	Cys	Asp	Tyr	His	Ala	Lys	Phe	Asp
				325					330					335	
Ser	Val	Thr	Gly	Glu	Cys	Asp	Glu	Cys	Glu	Tyr	Leu	Asn	Arg	Gly	Lys
			340					345					350		
Asn	Gly	Cys	Ile	Phe	His	Asn	Ala	Thr	His	Cys	Gln	Ile	Cys	His	Ala
		355					360					365			
Val	Pro	Pro	Trp	Glu	Lys	Glu	Asn	Val	Ser	Asp	Phe	Asn	Asp	Phe	Asp
	370					375					380				
Asp	Cys	Asn	Lys	Glu	Gln										
385					390										

<210> 6

<211> 2211

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic construct

<400> 6

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gctcgagggtc	ttgtgcttcc	tgggtacaag	tatcttggtc	ctgggaacgg	ccttgataag	180
ggcgatcctg	tcaattttgc	tgacgaggtt	gcccagagagc	acgacctctc	ctaccagaaa	240
cagcttgagg	cgggcgataa	cccttacctc	aagtacaacc	acgcggacgc	agagtttcag	300
gagaaactcg	cttctgacac	ttcttttggg	ggaaaccttg	ggaaggctgt	tttccaggct	360
aaaaagagga	ttctcgaacc	tcttggcctg	gttgagacgc	cggataaaac	ggcgccctgcg	420
gcaaaaaaga	ggcctctaga	gcagagtcct	caagagccag	actcctcgag	cggagttggc	480
aagaaaggca	aacagcctgc	cagaaagaga	ctcaactttg	acgacgaacc	tggagccgga	540
gacgggcctc	ccccagaagg	accatcttcc	ggagctatgt	ctactgagac	tgaaatgcgt	600
gcagcagctg	gcggaaatgg	tggcgatgcg	ggacaagggtg	ccgagggagt	gggtaatgcc	660
tccggtgatt	ggcattgcga	ttccacttgg	tcagagagcc	acgtcaccac	cacctcaacc	720
cgcacctggg	tcctgccgac	ctacaacaac	cacctgtacc	tgcggtctcg	ctcgagcaac	780
gccagcgaca	ccttcaacgg	attctccacc	ccctggggat	actttgactt	taaccgcttc	840

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cactgccact tctcgccaag agactggcaa aggctcatca acaaccactg gggactgcgc      900
cccaaaagca tgcaagtccg catcttcaac atccaagtta aggaggtcac gacgtctaac      960
ggggagacga cgtatccaa caacctcacc agcacggtcc agatctttgc ggacagcacg    1020
tacgagctcc cgtacgtgat ggatgcaggt caggagggca gcttgccctcc tttccccaac    1080
gacgtgttca tgggtgcctca gtacgggtac tgcggactgg taaccggagg cagctctcaa    1140
aaccagacag acagaaatgc cttctactgt ctggagtact ttcccagcca gatgctgaga    1200
accggaacaa actttgagat ggtgtacaag tttgaaaacg tgcccttcca ctccatgtac    1260
gctcacagcc agagcctgga taggctgatg aaccgcgtgc tggaccagta cctgtgggag    1320
ctccagtcta ccacctctgg aggaactctc aaccagggca attcagccac caactttgcc    1380
aagctgacca aaacaaactt ttctggctac cgcaaaaact ggctcccggg gcccatgatg    1440
aagcagcaga gattctccaa gactgccagt caaaactaca agattcccca gggaagaaac    1500
aacagtctgc tccattatga gaccagaact accctcgacg gaagatggag caattttgcc    1560
ccgggaacgg ccatggcaac cgcagccaac gacgccaccg acttctctca ggcccagctc    1620
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acttcagaag atgaacttag ggccaccaac ccccgggaca ctgacctgtt tggccacctg    1740
gcaaccaacc agcaaaacgc caccaccgtt cctaccgtag acgacgtgga cggagtcggc    1800
gtgtaccceg gaatggtgtg gcaggacaga gacatttact accaagggcc catttgggccc    1860
aaaattccac acacggatgg acactttcac ccgtctctc tcattggcgg atttgactg    1920
aaaagcccgc ctccacaaat attcatcaaa aacactcctg taccgcgcaa tccgcgaacg    1980
accttctctc cggccagaat caacagcttc atcaccagat acagcaccgg acaggtggct    2040
gtcaaaatag aatgggaaat ccagaaggag cgggtccaaga gatggaaccc agaggtccag    2100
ttcacgtcca actacggagc acaggactcg cttctctggg ctcccgacaa cgccggagcc    2160
tacaagagac ccaggggccat tggatcccga tacctcacca accacctcta g          2211

```

<210> 7

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic construct

<400> 7

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Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Ser Ile Gly Asp
 1          5          10          15
Gly Phe Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
 20          25          30
Ala Asn Gln Gln Lys Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
 35          40          45
Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Asp Pro Val
 50          55          60
Asn Phe Ala Asp Glu Val Ala Arg Glu His Asp Leu Ser Tyr Gln Lys
 65          70          75          80
Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
 85          90          95
Ala Glu Phe Gln Glu Lys Leu Ala Ser Asp Thr Ser Phe Gly Gly Asn
100          105          110
Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro Leu
115          120          125
Gly Leu Val Glu Thr Pro Asp Lys Thr Ala Pro Ala Ala Lys Lys Arg
130          135          140
Pro Leu Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145          150          155          160
Lys Lys Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Asp Asp Glu
165          170          175
Pro Gly Ala Gly Asp Gly Pro Pro Pro Glu Gly Pro Ser Ser Gly Ala
180          185          190
Met Ser Thr Glu Thr Glu Met Arg Ala Ala Ala Gly Gly Asn Gly Gly
195          200          205

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Asp	Ala	Gly	Gln	Gly	Ala	Glu	Gly	Val	Gly	Asn	Ala	Ser	Gly	Asp	Trp	210	215	220
His	Cys	Asp	Ser	Thr	Trp	Ser	Glu	Ser	His	Val	Thr	Thr	Thr	Ser	Thr	225	230	235
Arg	Thr	Trp	Val	Leu	Pro	Thr	Tyr	Asn	Asn	His	Leu	Tyr	Leu	Arg	Leu	245	250	255
Gly	Ser	Ser	Asn	Ala	Ser	Asp	Thr	Phe	Asn	Gly	Phe	Ser	Thr	Pro	Trp	260	265	270
Gly	Tyr	Phe	Asp	Phe	Asn	Arg	Phe	His	Cys	His	Phe	Ser	Pro	Arg	Asp	275	280	285
Trp	Gln	Arg	Leu	Ile	Asn	Asn	His	Trp	Gly	Leu	Arg	Pro	Lys	Ser	Met	290	295	300
Gln	Val	Arg	Ile	Phe	Asn	Ile	Gln	Val	Lys	Glu	Val	Thr	Thr	Ser	Asn	305	310	315
Gly	Glu	Thr	Thr	Val	Ser	Asn	Asn	Leu	Thr	Ser	Thr	Val	Gln	Ile	Phe	325	330	335
Ala	Asp	Ser	Thr	Tyr	Glu	Leu	Pro	Tyr	Val	Met	Asp	Ala	Gly	Gln	Glu	340	345	350
Gly	Ser	Leu	Pro	Pro	Phe	Pro	Asn	Asp	Val	Phe	Met	Val	Pro	Gln	Tyr	355	360	365
Gly	Tyr	Cys	Gly	Leu	Val	Thr	Gly	Gly	Ser	Ser	Gln	Asn	Gln	Thr	Asp	370	375	380
Arg	Asn	Ala	Phe	Tyr	Cys	Leu	Glu	Tyr	Phe	Pro	Ser	Gln	Met	Leu	Arg	385	390	395
Thr	Gly	Asn	Asn	Phe	Glu	Met	Val	Tyr	Lys	Phe	Glu	Asn	Val	Pro	Phe	405	410	415
His	Ser	Met	Tyr	Ala	His	Ser	Gln	Ser	Leu	Asp	Arg	Leu	Met	Asn	Pro	420	425	430
Leu	Leu	Asp	Gln	Tyr	Leu	Trp	Glu	Leu	Gln	Ser	Thr	Thr	Ser	Gly	Gly	435	440	445
Thr	Leu	Asn	Gln	Gly	Asn	Ser	Ala	Thr	Asn	Phe	Ala	Lys	Leu	Thr	Lys	450	455	460
Thr	Asn	Phe	Ser	Gly	Tyr	Arg	Lys	Asn	Trp	Leu	Pro	Gly	Pro	Met	Met	465	470	475
Lys	Gln	Gln	Arg	Phe	Ser	Lys	Thr	Ala	Ser	Gln	Asn	Tyr	Lys	Ile	Pro	485	490	495
Gln	Gly	Arg	Asn	Asn	Ser	Leu	Leu	His	Tyr	Glu	Thr	Arg	Thr	Thr	Leu	500	505	510
Asp	Gly	Arg	Trp	Ser	Asn	Phe	Ala	Pro	Gly	Thr	Ala	Met	Ala	Thr	Ala	515	520	525
Ala	Asn	Asp	Ala	Thr	Asp	Phe	Ser	Gln	Ala	Gln	Leu	Ile	Phe	Ala	Gly	530	535	540
Pro	Asn	Ile	Thr	Gly	Asn	Thr	Thr	Thr	Asp	Ala	Asn	Asn	Leu	Met	Phe	545	550	555
Thr	Ser	Glu	Asp	Glu	Leu	Arg	Ala	Thr	Asn	Pro	Arg	Asp	Thr	Asp	Leu	565	570	575
Phe	Gly	His	Leu	Ala	Thr	Asn	Gln	Gln	Asn	Ala	Thr	Thr	Val	Pro	Thr	580	585	590
Val	Asp	Asp	Val	Asp	Gly	Val	Gly	Val	Tyr	Pro	Gly	Met	Val	Trp	Gln	595	600	605
Asp	Arg	Asp	Ile	Tyr	Tyr	Gln	Gly	Pro	Ile	Trp	Ala	Lys	Ile	Pro	His	610	615	620
Thr	Asp	Gly	His	Phe	His	Pro	Ser	Pro	Leu	Ile	Gly	Gly	Phe	Gly	Leu	625	630	635
Lys	Ser	Pro	Pro	Pro	Gln	Ile	Phe	Ile	Lys	Asn	Thr	Pro	Val	Pro	Ala	645	650	655
Asn	Pro	Ala	Thr	Thr	Phe	Ser	Pro	Ala	Arg	Ile	Asn	Ser	Phe	Ile	Thr	660	665	670
Gln	Tyr	Ser	Thr	Gly	Gln	Val	Ala	Val	Lys	Ile	Glu	Trp	Glu	Ile	Gln	675	680	685



Lys	Glu	Arg	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Val	Gln	Phe	Thr	Ser	Asn
690						695					700				
Tyr	Gly	Ala	Gln	Asp	Ser	Leu	Leu	Trp	Ala	Pro	Asp	Asn	Ala	Gly	Ala
705					710					715					720
Tyr	Lys	Glu	Pro	Arg	Ala	Ile	Gly	Ser	Arg	Tyr	Leu	Thr	Asn	His	Leu
				725					730					735	

<210> 8  
 <211> 1803  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note=synthetic  
 construct

<400> 8

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cctggagccg	gagacgggccc	tccccagaa	ggaccatctt	ccggagctat	gtctactgag	180
actgaaatgc	gtgcagcagc	tggcggaat	gggtggcgatg	cgggacaagg	tgccgagggga	240
gtgggtaatg	cctccggtga	ttggcattgc	gattccactt	ggtcagagag	ccacgtcacc	300
accacctcaa	cccgacactg	ggtcctgccc	acctacaaca	accacctgta	cctgcggctc	360
ggctcgagca	acgccagcga	caccttcaac	ggattctcca	ccccctgggg	atactttgac	420
tttaaccgct	tccactgcca	cttctcgcca	agagactggc	aaaggctcat	caacaaccac	480
tggggactgc	gccccaaaag	catgcaagtc	cgcattctta	acatccaagt	taaggaggtc	540
acgacgtcta	acggggagac	gaccgtatcc	aacaacctca	ccagcacggg	ccagatcttt	600
gcggaacgca	cgtacgagct	cccgtacgtg	atggatgcag	gtcaggaggg	cagcttgccct	660
cctttcccca	acgacgtggt	catgggtgct	cagtacgggt	actgcggact	ggtaaccgga	720
ggcagctctc	aaaaccagac	agacagaaat	gccttctact	gtctggagta	ctttccagc	780
cagatgctga	gaaccggaaa	caactttgag	atgggtgtaca	agtttgaaaa	cgtgcccttc	840
cactccatgt	acgctcacag	ccagagcctg	gataggctga	tgaaccgct	gctggaccag	900
tacctgtggg	agctccagtc	taccacctct	ggaggaactc	tcaaccaggg	caattcagcc	960
accaactttg	ccaagctgac	caaaacaaac	ttttctgggt	accgcaaaaa	ctggctcccc	1020
gggcccata	tgaagcagca	gagattctcc	aagactgcca	gtcaaaaacta	caagattccc	1080
cagggaagaa	acaacagtct	gtccattat	gagaccagaa	ctaccctcga	cgaagatgg	1140
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caggcccagc	tcatctttgc	ggggcccaac	atcacgggca	acaccaccac	agatgccaat	1260
aacctgatgt	tactttcaga	agatgaactt	agggccacca	acccccggga	cactgacctg	1320
tttggccacc	tggaaccaa	ccagcaaaac	gccaccaccg	ttcctaccgt	agacgacgtg	1380
gacggagtcg	gcgtgtaccc	gggaatggtg	tggcaggaca	gagacattta	ctaccaaggg	1440
cccatttggtg	ccaaaattcc	acacacggat	ggacactttc	acccgtcttc	tctcattggc	1500
ggattttggac	tgaaaagccc	gcctccacaa	atattcatca	aaaacactcc	tgtaccgcgc	1560
aatcccgcga	cgaccttctc	tccggccaga	atcaacagct	tcatcaccca	gtacagcacc	1620
ggacaggtgg	ctgtcaaaaat	agaatgggaa	atccagaagg	agcgggtcaa	gagatggaac	1680
ccagaggtcc	agttcacgtc	caactacgga	gcacaggact	cgcttctctg	ggctcccgcac	1740
aacgcccggag	cctacaaaaga	gcccaggggc	attggatccc	gatacctcac	caaccacctc	1800
tag						1803

<210> 9  
 <211> 600  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note=synthetic  
 construct

<400> 9

Thr	Ala	Pro	Ala	Ala	Lys	Lys	Arg	Pro	Leu	Glu	Gln	Ser	Pro	Gln	Glu
1					5				10					15	

Pro	Asp	Ser	Ser	Ser	Gly	Val	Gly	Lys	Lys	Gly	Lys	Gln	Pro	Ala	Arg	
			20					25					30			
Lys	Arg	Leu	Asn	Phe	Asp	Asp	Glu	Pro	Gly	Ala	Gly	Asp	Gly	Pro	Pro	
		35					40					45				
Pro	Glu	Gly	Pro	Ser	Ser	Gly	Ala	Met	Ser	Thr	Glu	Thr	Glu	Met	Arg	
		50				55					60					
Ala	Ala	Ala	Gly	Gly	Asn	Gly	Gly	Asp	Ala	Gly	Gln	Gly	Ala	Glu	Gly	
65					70					75					80	
Val	Gly	Asn	Ala	Ser	Gly	Asp	Trp	His	Cys	Asp	Ser	Thr	Trp	Ser	Glu	
				85					90					95		
Ser	His	Val	Thr	Thr	Thr	Ser	Thr	Arg	Thr	Trp	Val	Leu	Pro	Thr	Tyr	
			100					105					110			
Asn	Asn	His	Leu	Tyr	Leu	Arg	Leu	Gly	Ser	Ser	Asn	Ala	Ser	Asp	Thr	
		115					120					125				
Phe	Asn	Gly	Phe	Ser	Thr	Pro	Trp	Gly	Tyr	Phe	Asp	Phe	Asn	Arg	Phe	
	130					135					140					
His	Cys	His	Phe	Ser	Pro	Arg	Asp	Trp	Gln	Arg	Leu	Ile	Asn	Asn	His	
145					150					155					160	
Trp	Gly	Leu	Arg	Pro	Lys	Ser	Met	Gln	Val	Arg	Ile	Phe	Asn	Ile	Gln	
				165					170					175		
Val	Lys	Glu	Val	Thr	Thr	Ser	Asn	Gly	Glu	Thr	Thr	Val	Ser	Asn	Asn	
			180					185					190			
Leu	Thr	Ser	Thr	Val	Gln	Ile	Phe	Ala	Asp	Ser	Thr	Tyr	Glu	Leu	Pro	
	195						200					205				
Tyr	Val	Met	Asp	Ala	Gly	Gln	Glu	Gly	Ser	Leu	Pro	Pro	Phe	Pro	Asn	
	210					215					220					
Asp	Val	Phe	Met	Val	Pro	Gln	Tyr	Gly	Tyr	Cys	Gly	Leu	Val	Thr	Gly	
225					230					235					240	
Gly	Ser	Ser	Gln	Asn	Gln	Thr	Asp	Arg	Asn	Ala	Phe	Tyr	Cys	Leu	Glu	
				245					250					255		
Tyr	Phe	Pro	Ser	Gln	Met	Leu	Arg	Thr	Gly	Asn	Asn	Phe	Glu	Met	Val	
			260					265					270			
Tyr	Lys	Phe	Glu	Asn	Val	Pro	Phe	His	Ser	Met	Tyr	Ala	His	Ser	Gln	
	275						280					285				
Ser	Leu	Asp	Arg	Leu	Met	Asn	Pro	Leu	Leu	Asp	Gln	Tyr	Leu	Trp	Glu	
	290					295					300					
Leu	Gln	Ser	Thr	Thr	Ser	Gly	Gly	Thr	Leu	Asn	Gln	Gly	Asn	Ser	Ala	
305					310						315				320	
Thr	Asn	Phe	Ala	Lys	Leu	Thr	Lys	Thr	Asn	Phe	Ser	Gly	Tyr	Arg	Lys	
				325					330					335		
Asn	Trp	Leu	Pro	Gly	Pro	Met	Met	Lys	Gln	Gln	Arg	Phe	Ser	Lys	Thr	
			340					345					350			
Ala	Ser	Gln	Asn	Tyr	Lys	Ile	Pro	Gln	Gly	Arg	Asn	Asn	Ser	Leu	Leu	
	355						360					365				
His	Tyr	Glu	Thr	Arg	Thr	Thr	Leu	Asp	Gly	Arg	Trp	Ser	Asn	Phe	Ala	
	370					375					380					
Pro	Gly	Thr	Ala	Met	Ala	Thr	Ala	Ala	Asn	Asp	Ala	Thr	Asp	Phe	Ser	
385					390					395					400	
Gln	Ala	Gln	Leu	Ile	Phe	Ala	Gly	Pro	Asn	Ile	Thr	Gly	Asn	Thr	Thr	
				405					410					415		
Thr	Asp	Ala	Asn	Asn	Leu	Met	Phe	Thr	Ser	Glu	Asp	Glu	Leu	Arg	Ala	
			420					425					430			
Thr	Asn	Pro	Arg	Asp	Thr	Asp	Leu	Phe	Gly	His	Leu	Ala	Thr	Asn	Gln	
	435						440					445				
Gln	Asn	Ala	Thr	Thr	Val	Pro	Thr	Val	Asp	Asp	Val	Asp	Gly	Val	Gly	
	450					455					460					
Val	Tyr	Pro	Gly	Met	Val	Trp	Gln	Asp	Arg	Asp	Ile	Tyr	Tyr	Gln	Gly	
465					470					475					480	
Pro	Ile	Trp	Ala	Lys	Ile	Pro	His	Thr	Asp	Gly	His	Phe	His	Pro	Ser	
				485					490					495		

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Pro Leu Ile Gly Gly Phe Gly Leu Lys Ser Pro Pro Pro Gln Ile Phe
      500                      505                      510
Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala Thr Thr Phe Ser Pro
      515                      520                      525
Ala Arg Ile Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ala
      530                      535                      540
Val Lys Ile Glu Trp Glu Ile Gln Lys Glu Arg Ser Lys Arg Trp Asn
545                      550                      555                      560
Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Ala Gln Asp Ser Leu Leu
      565                      570                      575
Trp Ala Pro Asp Asn Ala Gly Ala Tyr Lys Glu Pro Arg Ala Ile Gly
      580                      585                      590
Ser Arg Tyr Leu Thr Asn His Leu
      595                      600

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<210> 10

<211> 1617

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic  
construct

<400> 10

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tcaaccgcga cctgggtcct gccgacctac aacaaccacc tgtacctgcg gctcggctcg      180
agcaacgcga gcgacacctt caacggattc tccacccctt ggggatactt tgactttaac      240
cgcttccact gccactttct gccaaagagc tggcaaaggc tcatcaacaa ccactgggga      300
ctgcgccccca aaagcatgca agtccgcctc ttcaacatcc aagttaagga ggtcacgacg      360
tctaaccgggg agacgaccgt atccaacaac ctccaccagc cgggtccagat ctttgcggac      420
agcacgtacg agctcccgtc cgtgatggat gcagggtcagg agggcagctt gcctcctttc      480
cccaacgacg tgttcatggt gcctcagtac ggggtactgcg gactggtaac cggaggcagc      540
tctcaaaaacc agacagacag aaatgccttc tactgtcttg agtactttcc cagccagatg      600
ctgagaaccg gaaacaactt tgagatgggt tacaagtttg aaaacgtgcc cttccactcc      660
atgtacgctc acagccagag cctggatagg ctgatgaacc cgctgctgga ccagtacctg      720
tgggagctcc agtctaccac ctctggagga actctcaacc agggcaattc agccaccaac      780
tttgccaagc tgaccaaaaac aaacttttct ggctaccgca aaaactggct cccggggccc      840
atgatgaagc agcagagatt ctccaagact gccagtcaaa actacaagat tccccaggga      900
agaaacaaca gtctgctcca ttatgagacc agaactacc tgcacggaag atggagcaat      960
tttgccccgg gaacggccat ggcaaccgca gccaacgacg ccaccgactt ctctcaggcc      1020
cagctcatct ttgcggggcc caacatcacc ggcaacacca ccacagatgc caataacctg      1080
atgttcaact cagaagatga acttagggcc accaaccccc gggacactga cctgtttggc      1140
cacctggcaa ccaaccagca aaacgccacc accgttctta ccgtagacga cgtggacgga      1200
gtcggcggtg acccggaat ggtgtggcag gacagagaca ttactacca agggccatt      1260
tgggccaata ttccacacac ggatggacac ttccaccgtt ctctctcat tggcggattt      1320
ggactgaaaa gccgcctcc acaaattatc atcaaaaaca ctctgtacc cgccaatccc      1380
gcaacgacct tctctccggc cagaatcaac agcttcatca ccagtagacg caccggacag      1440
gtggctgtca aaatagaatg ggaaatccag aaggagcggt ccaagagatg gaaccagag      1500
gtccagttca cgtccaacta cggagcacag gactcgcttc tctgggctcc cgacaacgcc      1560
ggagcctaca aagagcccag ggccattgga tcccgatacc tcaccaacca cctctag      1617

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<210> 11

<211> 538

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic  
construct

&lt;400&gt; 11

Met	Arg	Ala	Ala	Ala	Gly	Gly	Asn	Gly	Gly	Asp	Ala	Gly	Gln	Gly	Ala
1				5					10					15	
Glu	Gly	Val	Gly	Asn	Ala	Ser	Gly	Asp	Trp	His	Cys	Asp	Ser	Thr	Trp
			20					25					30		
Ser	Glu	Ser	His	Val	Thr	Thr	Thr	Ser	Thr	Arg	Thr	Trp	Val	Leu	Pro
		35					40					45			
Thr	Tyr	Asn	Asn	His	Leu	Tyr	Leu	Arg	Leu	Gly	Ser	Ser	Asn	Ala	Ser
	50					55					60				
Asp	Thr	Phe	Asn	Gly	Phe	Ser	Thr	Pro	Trp	Gly	Tyr	Phe	Asp	Phe	Asn
65				70						75					80
Arg	Phe	His	Cys	His	Phe	Ser	Pro	Arg	Asp	Trp	Gln	Arg	Leu	Ile	Asn
			85						90					95	
Asn	His	Trp	Gly	Leu	Arg	Pro	Lys	Ser	Met	Gln	Val	Arg	Ile	Phe	Asn
			100					105					110		
Ile	Gln	Val	Lys	Glu	Val	Thr	Thr	Ser	Asn	Gly	Glu	Thr	Thr	Val	Ser
		115					120					125			
Asn	Asn	Leu	Thr	Ser	Thr	Val	Gln	Ile	Phe	Ala	Asp	Ser	Thr	Tyr	Glu
	130					135					140				
Leu	Pro	Tyr	Val	Met	Asp	Ala	Gly	Gln	Glu	Gly	Ser	Leu	Pro	Pro	Phe
145				150						155					160
Pro	Asn	Asp	Val	Phe	Met	Val	Pro	Gln	Tyr	Gly	Tyr	Cys	Gly	Leu	Val
			165						170					175	
Thr	Gly	Gly	Ser	Ser	Gln	Asn	Gln	Thr	Asp	Arg	Asn	Ala	Phe	Tyr	Cys
		180					185						190		
Leu	Glu	Tyr	Phe	Pro	Ser	Gln	Met	Leu	Arg	Thr	Gly	Asn	Asn	Phe	Glu
	195						200					205			
Met	Val	Tyr	Lys	Phe	Glu	Asn	Val	Pro	Phe	His	Ser	Met	Tyr	Ala	His
	210					215					220				
Ser	Gln	Ser	Leu	Asp	Arg	Leu	Met	Asn	Pro	Leu	Leu	Asp	Gln	Tyr	Leu
225				230						235					240
Trp	Glu	Leu	Gln	Ser	Thr	Thr	Ser	Gly	Gly	Thr	Leu	Asn	Gln	Gly	Asn
			245					250						255	
Ser	Ala	Thr	Asn	Phe	Ala	Lys	Leu	Thr	Lys	Thr	Asn	Phe	Ser	Gly	Tyr
		260					265						270		
Arg	Lys	Asn	Trp	Leu	Pro	Gly	Pro	Met	Met	Lys	Gln	Gln	Arg	Phe	Ser
	275						280					285			
Lys	Thr	Ala	Ser	Gln	Asn	Tyr	Lys	Ile	Pro	Gln	Gly	Arg	Asn	Asn	Ser
	290					295					300				
Leu	Leu	His	Tyr	Glu	Thr	Arg	Thr	Thr	Leu	Asp	Gly	Arg	Trp	Ser	Asn
305				310						315					320
Phe	Ala	Pro	Gly	Thr	Ala	Met	Ala	Thr	Ala	Ala	Asn	Asp	Ala	Thr	Asp
			325					330						335	
Phe	Ser	Gln	Ala	Gln	Leu	Ile	Phe	Ala	Gly	Pro	Asn	Ile	Thr	Gly	Asn
		340					345						350		
Thr	Thr	Thr	Asp	Ala	Asn	Asn	Leu	Met	Phe	Thr	Ser	Glu	Asp	Glu	Leu
		355					360					365			
Arg	Ala	Thr	Asn	Pro	Arg	Asp	Thr	Asp	Leu	Phe	Gly	His	Leu	Ala	Thr
	370					375					380				
Asn	Gln	Gln	Asn	Ala	Thr	Thr	Val	Pro	Thr	Val	Asp	Asp	Val	Asp	Gly
385				390						395					400
Val	Gly	Val	Tyr	Pro	Gly	Met	Val	Trp	Gln	Asp	Arg	Asp	Ile	Tyr	Tyr
			405						410					415	
Gln	Gly	Pro	Ile	Trp	Ala	Lys	Ile	Pro	His	Thr	Asp	Gly	His	Phe	His
		420						425					430		
Pro	Ser	Pro	Leu	Ile	Gly	Gly	Phe	Gly	Leu	Lys	Ser	Pro	Pro	Pro	Gln
		435					440					445			
Ile	Phe	Ile	Lys	Asn	Thr	Pro	Val	Pro	Ala	Asn	Pro	Ala	Thr	Thr	Phe
	450					455					460				

Ser Pro Ala Arg Ile Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln  
 465 470 475 480  
 Val Ala Val Lys Ile Glu Trp Glu Ile Gln Lys Glu Arg Ser Lys Arg  
 485 490 495  
 Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Ala Gln Asp Ser  
 500 505 510  
 Leu Leu Trp Ala Pro Asp Asn Ala Gly Ala Tyr Lys Glu Pro Arg Ala  
 515 520 525  
 Ile Gly Ser Arg Tyr Leu Thr Asn His Leu  
 530 535

<210> 12  
 <211> 150  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence; note=synthetic  
 construct

<400> 12  
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 tcaaagagct gccagacgac ggccctctgg gccgtcgccc cccaatcga gccagcgaac 120  
 gagcgaacgc gacagggggg ggagtgccac 150

<210> 13  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note=synthetic  
 construct

<400> 13  
 ctctagcaag ggggttttgt 20

<210> 14  
 <211> 7  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note=synthetic  
 construct

<400> 14  
 agtgtgg 7

<210> 15  
 <211> 158  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note=synthetic  
 construct

<400> 15  
 aggtgggtgat gtcattgttg atgtcattat agttgtcacg cgatagttaa tgattaacag 60  
 tcatgtgatg tgtgttatcc aataggatga aagcgcgcga atgagatctc gcgagacttc 120

cggggtataa aaggggtgag tgaacgagcc cgccgcca 158

<210> 16  
 <211> 112  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note=synthetic  
 construct

<400> 16  
 ggtggattct gggatatatt ccgcctacct gctgccgaag gtccaaccag agcttcagtg 60  
 ggcgtggact aacctcgaag agtataaatt ggccgccctc aatctggagg ag 112

<210> 17  
 <211> 169  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note=synthetic  
 construct

<400> 17  
 agtcaaagac ttttttgctt gggcaaaggt caaccaggtg ccggtgactc acgagtttat 60  
 ggttcccaag aaagtggcgg gaactgagag ggcggagact tctagaaaac gcccactgga 120  
 tgacgtcacc aataccaact ataaaagtcc ggagaagcgg gcccggtc 169

<210> 18  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note=synthetic  
 construct

<400> 18  
 Gly Ser Ser Asn Ala Ser Asp Thr  
 1 5

<210> 19  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note=synthetic  
 construct

<400> 19  
 Thr Thr Ser Gly Gly Thr Leu Asn Gln Gly Asn Ser Ala Thr  
 1 5 10

<210> 20  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic  
construct

<400> 20

Asn Gly Arg Ala His Ala  
1 5

<210> 21

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic  
construct

<400> 21

Ser Ile Gly Tyr Pro Leu Pro  
1 5

<210> 22

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic  
construct

<400> 22

Lys Phe Asn Lys Pro Phe Val Phe Leu Ile  
1 5 10

<210> 23

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic  
construct

<400> 23

Asn Ile Ser Leu Asp Asn Pro Leu Glu Asn Pro Ser Ser Leu Phe Asp  
1 5 10 15  
Leu Val Ala Arg Ile Lys  
20